

New U.S. Patent Application Inventors: R. JURECIC et al. Title: HEPP, A Novel Gene with a Role in Hematopoietic and Neural Development" Attorney Docket No. 39532.176599 Sheet 1 of 14

FIGURE 1A

1	CCCCGC	GTCG	GTC'	TTC	CACC	TCAC	CCTT	TCGI	AGCI	GGC	CGC	CCGC	CTTC	GCT(GTG	CGC	AGT'	ΓTC	60
61	GGGGGA	CTGG	ACC'	TTC	CCTG	GCTT	ATT	GCAC	GCGC	CGA	\GCC	GCC	ATGO	GCG/	ACC	CTT'	TGC'	rgg	120
	GCAGGT																		180
181	CCTGGA	CAGG	ATG	TTTC	GCTA	GAGG	GCT	GAA	BAGG	AAA	CAT	rggi	rga(CCA	GGA.	AGA	AGG	AGT	240
1				_	A R	-	L	K		K	Y	G	D	Q	E	E	G	V	17
241	AGAGGG'	TTTT	GGC.	ACT(GTCC							ACAC	GTC!	ACT	CCT	GGA	CAT	GTC	300
	E G	F	_	_	V P		Y	S	L	Q	R	Q	S	L	L	D	M	S	37
301	CCTTGT																		360
	r A	ĸ		-	ьc		M	L	V	E	P	N	L	C	R	S	V	L	57
361	CATCGC																		420
	IA	N	_		R C	-	Q	E	E	M	S	Q	D	G 	v 	W	H	G	77
421	GATGGC																		480
	M A	P 	~		V I		A	P	V	E	R	L	V	S	T	E	I	L	97
481	GTGTCG																		540
	C R	T			G A		E	E	H	P	A	P	E	L	E	D NAC	A Car	P	117
541	CTTGCA						P		V	G	S	AGCA A	P	G G	GCA O	AAG R	GAA N	P	600 137
CO1	L Q TCAGAG	N			SE		-	I						_	_			_	660
601	O S	S			GAGA E M		ACAG S	P	Q Q	E E	N.	R.	G G	AAG S	F	0	K	S	157
661	ACTGGA	_	_						_				_		_	~		_	720
001	L D	O			GAGA E 1		E	N	K	N	S	S	S	V	E	E	L	F	177
721	CTCAGA	~					_					-	-	-			_	-	780
721	S D	V			s Y		D	L	D	T	V	L L	T	G	M	м	S	G	197
781	GACCAA		_	_									•	-				_	840
,01					1001			1011											
	T K	S	S	L (C N	1 G	L	E	G	F	Α	A	Α	т	P	P	P	S	217
841	T K	S TTGC	_		C N	_	L CTGA	E GCT	G GGAC	F CCAT				_	_	_	_		
841	T K TTCCAC S T	_	CAAG	TCT		CTGG								_	_	_	_		217 900 237
	TTCCAC S T	TTGC	CAAG K	TCT(GACC D I	CTGG	CTGA E	GCT(GGA(CCAT H	rgt(GGT/	AGA(GAT I	TCT L	GGT V	GGA E	GAC T	900
	TTCCAC	TTGC	CAAG K	TCT(GACC D I	CTGG	CTGA E	GCT(GGA(CCAT H	rgt(GGT/	AGA(GAT I	TCT L	GGT V	GGA E	GAC T	900 237
901	TTCCAC s T CTGAGA	TTGC C .GGCC	CAAG K CACC	TCT(S :	GACC D I	CTGGG A GGCT	CTGA E AAGG	GCTG	GGA(D AGG(CCAT	rgt(v CCA(GGTZ V GTC	AGA(E CCC	GAT I ATG	TCT L GAG	GGT V CTC	GGA E ACG	GAC T TGT	900 237
901 961	TTCCAC S T CTGAGA	TTGC C .GGCC	CAAG K CACC	TCT(S :	GACC D I GTGC	CTGG(A GGCTA	CTGA E AAGG	GCTG L GTGZ	GGAC D AGGC	CCAT H CCAC	rgto V CCAO	GGTZ V GTCG	AGAG E CCC	GAT I ATG GGC	TCT L GAG TCT	GGT V CTC	GGA E ACG GCT	GAC T TGT CAT	900 237 960
901 961 1021	TTCCAC S T CTGAGA * GTTGTG	TTGC C GGCC	CAAG K CACC CAGA	TCT(S) CCA(GAC.	GACC D I GTGC AGAT	CTGG(A GGCTA FAAG(GGAC'	CTGA E AAGG CACT	GCTO L GTGZ TGTO	GGAC D AGGC CCTA GGAC	CCAT H CCAC AAGA GGAT	TGT(V CCA(AGG(GGTA V GTCA GGCTA TGTA	AGAG E CCC TCT GTC	GAT I ATG GGC ACA	TCT L GAG TCT GCT	GGT V CTC TGA ATG	GGA E ACG GCT TCT	GAC T TGT CAT AGT	900 237 960 1020
901 961 1021 1081	TTCCAC S T CTGAGA * GTTGTG TATCCT	TTGC C GGCC ACCC	CAAG K CACC CAGA STGT	TCT(S)	GACC D I GTGC AGAT ATTC AGGT	CTGGG A GGCTA GAAGG GGAAG	CTGA E AAGG CACT CCAC	GCT(L GTG; TGT(TGT(GGA(D AGG(CCTA GGA(AAA)	CCAT H CCAC AAGA GGAT	rgto V CCA AGG rGG AGT	GGTA V GTCC GGCT TGTC	AGAG E CCC TCT GTC ATA	GAT I ATG GGC ACA TGT	TCT L GAG TCT GCT TTT	GGT V CTC TGA ATG	GGA E ACG GCT TCT GCA	GAC T TGT CAT AGT	900 237 960 1020 1080
901 961 1021 1081 1141	TTCCAC S T CTGAGA * GTTGTG TATCCT CTATTT	TTGC C GGCC ACCC TTTTC	CAAG K CACC CAGA STGT ATTA AAGA	GAC.	GACC D I GTGC AGAT ATTC AGGT ATTT	CTGGC A A GGCTA GGAGT GGAGT GGAGT GTTTT	ETGA E AAGG CACT FCAC CTTT AAAAC	GCT(L GTGZ TGT(TGT(CTAL CTTTT	GGAC D AGGC CCTA GGAC AAA1	ECAT H CCAC AAGA EGAT TTAA	rgto V CCAO AGGO rgg' AGT'	GGTA V GTCC GGCT TGTC	AGAO E CCC ICT GTC ATA	GAT I ATG GGC ACA TGT TTT	TCT L GAG TCT GCT TTT TCA	GGT V CTC TGA ATG TGG GCT	GGA E ACG GCT TCT GCA	GAC T TGT CAT AGT ATA TTC	900 237 960 1020 1080 1140
901 961 1021 1081 1141 1201 1261	TTCCAC S T CTGAGA * GTTGTG TATCCT CTATTT TTTTGT TTAAAA AAATAC	TTGC C GGCC ACCC TTTC TCAA CTTA	CAAG K CACC CAGA GTGT ATTA AAGA FATT	GAC. GAT. TTTT	GACC D I GTGC AGAT ATTC AGGT ATTT TCTA	CTGGC A A GGCTA FAAGC GGAC TTTTA ACAA	ETGA EAAGG CACT CCACT AAAC AAAG	GCTC L GTGTC CTGTC CTAL CTTTT CCTC	GGAC D AGGC CCTA GGAC AAAT CTGC	CCAT H CCAC AAGA GGAT TACT CTGC ATAC	rgto v CCAO AGGO rgg: AGT' rtta CTAO	GGTA V GTCO GGCT TTTA AGA CATT	AGAGECCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	GAT I ATG GGC ACA TGT TTT AAA	TCT L GAG TCT GCT TTT TCA CAT	GGT V CTC TGA ATG TGG GCT TTA	GGA E ACG GCT TCT GCA ATT TAA	GAC T TGT CAT AGT ATA TTC CCT GTC	900 237 960 1020 1080 1140 1200 1260 1320
901 961 1021 1081 1141 1201 1261	TTCCAC S T CTGAGA * GTTGTG TATCCT CTATTT TTTTGT TTAAAA AAATAC TCTACA	TTGC C GGCC ACCC TTTTC TCAA CTTA GTAT	CAAG CAGA CAGA CAGA CATTA CAGA CATT CGGT CCAA	GAC. GAC. GAT. TTTT	GACC D I GTGC AGAT ATTC AGGT TCTA TCAT AACT	CTGGC A GGCTA FGAAG FGAAG FTTTA ACAAA FTTTA	ETGA EAAGG CACT TCAC CTTT AAAC ACAT AAAG	GCTG L GTGTG CTA CTA CCTA CCTG GTT CCTG	GGAC D AGGC CCTA GGAC AAAT TTAT CTGC TAAA	ECATO	rgto V Aggo rgg Agt Agt rtta Cta Gaa	GGTA V GGC' TGTA AGA' CAT' AAC' TGT'	AGAGECCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	GAT I ATG GGC ACA TGT TTT AAA TTTT CAT	TCT L GAG TCT GCT TTCA CAT TGT	GGT V CTC TGA ATG GCT TTA TAC AGG	GGA E ACG GCT TCT GCA ATT TAA TGA CTC	GAC T TGT CAT AGT ATA TTC CCT GTC CAG	900 237 960 1020 1080 1140 1200 1260 1320 1380
901 961 1021 1081 1141 1201 1261 1321 1381	TTCCAC S T CTGAGA * GTTGTG TATCCT CTATTT TTTTGT TTAAAA AAATAC TCTACA TATGGT	TTGC C GGCC TTTTC TCAA CTTA GTAT	CAAG CAGA	GAC. GAC. GAT. TTTT	GACC D I GTGC AGAT ATTC AGGT TCTA TCAT AACT GTAC	CTGGC A GGCTA GGAC GGAC GTTTA ACAA FTTTA TGTA GGAGC	CTGA E AAGG CACT CCACT AAAC ACAT AAAG	GCTC GTGTC TGTC TTGTC TTGTC CTA TTTT CCTC GTTC GTTA GTA G	GGAC D AGGC CCTA GGAC AAAT CTGC IAAA CCGC GAAC	H CCAC AAGA TTAA TACT CTGC ATAC CCAC	rgto V CCAC rgg: Agt: rtta CTAC BAA BGG:	GGTA V GTCO GGC' TGTO AGA' CAT' AAC' TGT' ACA	AGAGE E CCC. GTC. ATAGE TTCC TTAGE GCT	GAT I ATG GGC ACA TGT TTT AAA TTTT CAT	TCT L GAG TCT TCA TCA CAT GAG CTG	GGT V CTC TGA ATG GCT TTA CAGG	GGA E ACG GCT TCT GCA ATT TAA TGA CTC	GAC T TGT CAT AGT ATA TTC CCT GTC CAG CAC	900 237 960 1020 1080 1140 1260 1320 1380 1440
901 961 1021 1081 1141 1201 1261 1321 1381 1441	TTCCAC S T CTGAGA * GTTGTG TATCCT CTATTT TTTTGT TTAAAA AAATAC TCTACA TATGGT TGGGTC	TTGC C GGCC TTTTC TCAA CTTA GTAT GTAT CTTC CTTAC	CAAG CAGA CAGA CAGA CATTA CAGA CATT CGGT CCAA CATT	GAC. GAC. GAT. TTTT GTG GGC. GCTA	GACC D I GTGC AGAT ATTC AGGT TCTA TCAT AACT GTAC GATC	CTGGC A GGCTA GGAC GAAC GTTTA ACAAA FTTTA GGGAC CGGAC	ETGA E AAGG CACT CTTT AAAC ACAT AAAG AATG ATGA	GCTG GTGTG CTA CTA CCTG GTTGTG CCTG CCTC CCTC CCTC CCTC CCTC CCTC	GGAC D AGGC CCTA GGAC AAAT CTGC IAAA CCGC GAAC TCCT	CCAT H CCAC AAGA FTAA CTGC ATAC GCCC CCAC	rgto V CCAO AGGO AGT' FTTAO EAAA EGG' IGCAO CCCO	GGTA V GTCC GGC' TGTC AGA' CAT' AAC' TGTC ACAC CGTC	AGAGE E CCC. GTC. ATAGE TTC TTAGE GCTG	GAT I ATG GGC ACA TGT TTT AAA TTTT CAT CA	TCT L GAG TCT TCT TCA CAT TGT GAG CTG	GGT V CTC TGA ATG GCT TTA CAGG CCC	GGA E ACG GCT TCT GCA ATT TAA TGA CTC	GAC T TGT CAT AGT ATA TTC CCT GTC CAG CAC	900 237 960 1020 1080 1140 1260 1320 1380 1440 1500
901 961 1021 1081 1141 1201 1261 1321 1381 1441 1501	TTCCAC S T CTGAGA * GTTGTG TATCCT CTATTT TTTTGT TTAAAA AAATAC TCTACA TATGGT TGGGTC TATGCC	TTGC C GGCC TTTTC TCAA CTTA GTAT CTTC TCTAC TCTAC	CAAG CAGA GTGT ATTA AAGA CATT CGGT CCAA CATT	GAC. GAC. GAT. TAT. GTG GGC. GCTA	GACC D I GTGC AGAT ATTC AGGT ATTT TCTA TCAT AACT GTAC GATC	CTGGC A GGCTA GGAC GGAC GGAC GTTTA ACAA ACTTTA ACAA A	ETGA E AAGG CACT AAAC ACAT AAAG AATG GCTC	GCTG L GTGTG CTAL CTAL GTTGTG GTTG GTTG GTAG GTTG GTAG GTAG	GGAC D AGGC CCTA GGAC TTAT CCGC GAAC TCCT AGGC AGGC AGC A	CCAT H CCAC AAGA FTAA FACT CTGC ATAC CCAT CCAT	rgt(car)	GGTA GGCT GGCT AGA TGTC AGA TGTC AGA CGTC CGTC	AGAGE ECCC. TCTG GTC. ATA TTTG TAG. GTG GTG ACT	GAT I ATG GGC ACA TGT TTT CAT CCA CCA CCA CCC	TCT L GAG TCT TCA CAT GAG CTG GAG CTG	GGT V CTC TGA ATG GCT TTA CAGG CCC GGCT	GGA E ACG GCT TCT GCA ATT TAA TGA CTC	GAC T TGT CAT AGT ATA TTC CCT GTC CAG CAC ATT AAC	900 237 960 1020 1080 1140 1200 1320 1380 1440 1500 1560
901 961 1021 1081 1141 1201 1261 1321 1381 1441 1501 1561	TTCCAC S T CTGAGA * GTTGTG TATCCT CTATTT TTTTGT TTAAAA AAATAC TCTACA TATGGT TGGGTC ACCAGT	TTGC C GGCC ACCC TTTCA CTTA GTAT CTTCC TTGCT CTTAC CTT	CAAG K CACC CAGA GTGT ATTA AAGA FATT CGGT CCAA CATT FCTG	GAC. GAC. GAC. GAT. TTTT GTG GGC GGGA	GACC D I GTGC AGAT ATTC AGGT TCAT AACT GTAC GATC	CTGGC A GGCTA FGAAG FTTTA ACAAA FTTTA ACAAA FTTTA CGTA GGGA ATGCC	ETGA E AAGG CTTT AAAC ACAT AAAGG ATGA GCTC GAGG GAGG	GCTG GTGTG TGTG TGGG TGGG	GGAC AGGC AGGC AAAT CTGC FAAAC CCGC GAAC TCCT	H CCAC H AAGA AAGA TTAA TTAA CCTGC CCAC CCAC TTAG CCTTAA	rgt(v v cca(agg; rtta cta(cca(aga) recci	GGTA V GTCC GGC GGC GGC GGC GGC GGC GGC GGC GG	AGAGE E CCC.	GAT I ATG GGC ACA TGT TTT AAA TTT CAT CCA CCA CCT TTG	TCT L GAG TCT TCT TCA TCA TCA TCA TGAG GAG GAT TGAG GAT TGAG TCC	GGT V CTC TGA ATG GCT TTA CCC AGG CCC GGC AATT	GGA E ACG GCT TCT GCA ATT TAA TGA CTC CCT TTT CCCC	GAC T TGT CAT AGT ATA TTC CCT GTC CAG CAC ATT AAC ATC	900 237 960 1020 1080 1140 1200 1320 1380 1440 1500 1560 1620
901 961 1021 1081 1141 1201 1261 1321 1381 1441 1501 1561 1621	TTCCAC S T CTGAGA * GTTGTG TATCCT CTATTT TTTTGT TTAAAA AAATAC TCTACA TATGGT TGGGTC ACCAGT ACTGTC	TTGC C GGCC ACCC TTTCA CTTA GTAT CTTCC TTGCT TTGCT TTGCT TTGCT TTGCT	ZAAG K ZACC ZAGA ATTTA AAGA FATT FGGT FCTA FCTA FCTA FCTA FCTA FCTA	TCTC S CCA GAC GAC GAC GAC GAC GAC GAC GAC GAC	GACC D I GTGC AGAT ATTC AGGT TCAT AACT GTAC GTAC	CTGGC A GGCTA FGAAG FTTTA ACAAA FTTTA ACAAA FTTTA CGGAC CGGAC CTGTC ACCAC ACCA	ETGA E AAGG CACT CACT AAAC ACAT AAAG AATG GCTC CACT GAGG CATG	GCTO L GTGTO TGTO TGTO TGTO TGTA TGTO TCTA TCTA TCTA GGTT TGGA GCA GCA GCA GGTGA	GGAC D AGGC CCTA AGGC AAAAT CTGC GGAAC GGAAC GGAAC TTGC TTG	H CCAC H AAGA AAGA TTAA CCTGC CCAC TTAGC CCTTAGC CCTTAGG CCTTA	rgt(v v cca(agg) rtt; cta(cca(gaa) rgc; agg) rgc; agg)	GGTA V GTCC GGC GGC GGC GGC GGC GGC GGC GGC GG	AGAGE E CCCC	GAT I ATG GGC ACA TGT TTT AAA TTTT CCA CCA CCT TTG TGC	TCT L GAG TCT TCA TCA TCA TCA TCA TCA TCA TCA TCA	GGT V CTC TGA ATG GCT TTA CA AGG CCC GGC AAT TTG AAC AAC	GGA E ACG GCT TCT GCA ATT TAA TGA CTC CCT TTT CCC GCC	GAC T TGT CAT AGT ATA TTC CCT GTC CAG CAC ATT AAC ATC CCA	900 237 960 1020 1080 1140 1200 1320 1380 1440 1500 1560 1620 1680
901 961 1021 1081 1141 1201 1261 1321 1381 1441 1501 1561 1621 1681	TTCCAC S T CTGAGA * GTTGTG TATCCT CTATTT TTTTGT TTAAAA AAATAC TCTACA TATGGT TAGGT ACCAGT ACCAGT ACTGTC GCACCA	TTGC C GGCC ACCC TTTTC TCAA CTTAC CT	ZAAGA K ZACC ZAGA ZAGA ZAGA ZAGA ZAGA ZAGA ZAGA	TTCTC S S CCCA GAC. GAC. GAC. TAT. TTTT GGGG GGC. CCTA GGCG CCTA GGCA CCCA CCCA CCCA CCCA	GACCOLLA COLLARA COLLA	CTGGC A GGCTA FGAAG FTTTA ACAAA FTTTA GGAAG FTTTA GGAAG CGGAG ATGC AGCAG	ETGA E EAAAGG CACT CACT CACT CACT CACA AAAA AAAGG CACT CACT	GCTG L GGTG TGTG TGTG TGTG TGTG TGTG TG	GGAC D AGGC CCTA GGAC AAAT TTAT CTGC GGAAC TCCT AGCT CATC CA	HAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	rgt(V VCCA(AGG(Irgg' Irtt)	GGTA V GGCC GGCC TGTC TGTC AGA CAT AAC CGTC CGTC CAG CAG	AGAGE ECCC. TCTG GTC. ATAC TTTG GTTG GTG GTG ACT GCT GCT GCT GCT GCT GCT GCT GCT GCT G	GAT I ATG GGC ACA TGT TTT AAA TTT CCAT CCAG CCT TTG CCCC	TCT L GAG GCT TTT TCA CAT TGGAG GAT GGAG GAT CCGGAC CCGG	GGT V CTC TGA ATG TGG GCT TTA CCC AGG AATT TTG AACC CCT	GGA E ACG GCT TCT GCA ATT TAA TGA CTC CCT TTT CCCC GCC GCA GCG	GAC T TGT CAT AGT ATA TTC CCT GTC CAG CAC ATT AAC ATC CCA CTC	900 237 960 1020 1080 1140 1200 1320 1380 1440 1500 1560 1620 1680 1740
901 961 1021 1081 1141 1201 1261 1321 1381 1441 1501 1561 1621 1681 1741	TTCCAC S T CTGAGA * GTTGTG TATCCT CTATTT TTTTGT TTAAAA AAATAC TCTACA TATGGT TAGGT ACCAGT ACCAGT ACTGTC GCACCA AGAGAG	CTTGC CGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	ZAAG K ZACC ZAGA ZAGA ZATT TGGT TCAG TTAT TCAG TTCAG TTCC TCCC TC	TTCTC S S CCCA GAC. GAC. GAC. GAC. TAT. TTTT GGGG GGC CCTA GGCG CCTA CGCA CCCA CC	GACC GTGC AGAT ATTC AGGT TCTA AACT TCAA AACT TAAA CTGC CCCA GTCA CCCTA	CTGGGC AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	ETGA E EAAAGG CACT CACT CACT CACA AAAAC AAAAG CACT CACT	GCTG L GGTG TGTG TGTG TGTG TGTG TGTG TG	GGAC D AGGC CCTA GGAAAAT CCGC GGAAC TCCT CATC CATC GGGC GGGC CATC CGGC	CCATA H CCAC AAGA AAGA TTAA TTAC TTAC TTAC TTAC	V CCA AGGG TGT TGT TGT TGG TGG TG	GGTA V GGCC GGC	AGAGE ECCC. ICTG GTCG ATAC TTTG GTTG GTG ACT GTCG GTCG	GAT I ATG GGC ACA TGT TTT CAT CCA CCA CCT TGC CCC CCC	TCT L GAG GCT TTT TCA CAT TGT GGAG CTG GAT CCG CCG AGG	GGT V CTC TGA ATG TGG GCT TTA CCC AGG AAT TTG AGC CCT CTT	GGA E ACG GCT TCT GCA ATT TAA TGA CCT CCCT TTT CCC GCC GCG GCG GCG GCT	GAC T TGT CAT AGT ATA TTC CCT GTC CAG CAC ATT AAC ATC CCA CTC TGC	900 237 960 1020 1080 1140 1200 1380 1440 1500 1620 1680 1740 1800
901 961 1021 1081 1141 1201 1261 1321 1381 1441 1501 1561 1621 1681 1741 1801	TTCCAC S T CTGAGA * GTTGTG TATCCT CTATTT TTTTGT TTAAAA AAATAC TCTACA TATGGT TGGGTC ACCAGT ACTGTC GCACCA AGAGAG TTTTAA	TTGC C GGCC ACCC TTTC TCAA CTTAC CTAC CT	ZAAGA K ZACC K ZAGA ZAGA ZAGA ZAGA ZAGA ZAGA ZAGA ZA	TCTCTC S : CCCA GAC. GAC. GAC. GAC. GAC. GAC. GAC.	GACCOLORION CONTROL CO	CTGGGC AGGAC GGAC GGAC GGAC GGAC GGAC GG	ETGA E AAGG CACT CACT CACT CACA AAAC AAAAG CACAC CACT GAGG GAGG	GCTG L GGTG TGTG TGTG TGTG TGTG TGTG TG	GGAC D AGGC CCTA GGAC CCGC GGAC CCGC CCAT GGGC CCAT GGGC GGGC GGGC CCAT GGGC CCAT GGGC CCAT CCGC CCAT CCAT CCGC CCAT CCA	H CCAC H CCAC H AAGM AAGM CTAM CCTGC CCAC CCAC CCAC CCAC CCAC CCAC CCA	V AGGG AGGT TTT TTT TTT TTT TTT TTT TTT	GGTA V GTCA GGC GGC GGC GGC GGC GGC GGC GGC GGC G	AGAG E CCC ICTC GTC GTC TTAG TTAG GCT GTC GCT GTC GCT GTC GCT GCT GCT GC	GAT I ATG GGCACA TGT TTT CAT CCA CCA TGC CCC TTG CCC CCC TTCC	TCT L GAG TCT TTT TCA CAT TGT GAG CTG GAT CCG GAT TCC CCG AGG AGG ATA	GGT V CTC TGA ATG TGG GCT TTA CCC AGG CCC AAT TTG AAC CCT TTGA	GGA E ACG GCT TCT GCA ATT TAA TGA CCC CCT TTTT CCC GCC CCAC CCT TTTT	GAC T TGT CAT AGT ATA TTC CCT GTC CAG CAC ATT AAC ATC CCA CTC TGC AGG	900 237 960 1020 1080 1140 1200 1380 1440 1500 1620 1680 1740 1800 1860
901 961 1021 1081 1141 1201 1261 1321 1381 1441 1501 1561 1621 1681 1741 1801 1861	TTCCAC S T CTGAGA * GTTGTG TATCCT CTATTT TTTTGT TTAAAA AAATAC TCTACA TATGGT TGGGTC ACCAGT ACTGTC GCACCA AGAGAG TTTTAA GCTCCT	TTGC C GGCC TTTCA TCAA CTTA CTTA CTTA CT	CAAGA CAGA CAGA CAGA CAGA CAGA CAGA CAG	TCTC S S CCA GAC. GAC. GAC. GAT. TAT. TTTT GGG GGC CTA GGAC CAG CAG CAG CAG CAG CAG CAG CAG C	GACC GACC GACC AGAT AATT TCTA AACT GACC GACC CCCA GGCC GGCC GGAC GCC GGAC GCC GGAC GCC GGAC GGAC GCC GGAC GCC GGAC GCC GGAC GCC GGAC GCC GGAC GCC GCC GGAC GCC GCC GGAC GCC GCC	CTGGC A GGCT GGAC GGAC GTTT ACAA ACAA ATGC CTGT AGCA AGCA	ETGA E AAGG CACT TCAC CTTT AAAC ACAT AAAGG CACT GGCC CACT GGCC CACT GGCC CATGC	GCTG L GGTG CTAG CTAG CTAG CTAG CTAG CTAG CTAG	GGAC D AGGC CCTA GGAC AAAA TTA CCGC GAAC TCCT TGCC CATC CCATC CGGGC TGGC GGGC TTAAA	CCATA AAGA AAGA TTAA TAACT TA	V AGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GGTA V GTCC GGC TGTC AGA CCAT ACAC CCTC CCTG CCTG	AGAGE ECCC. ICTC GTC. ATA TTAG. TTAG. GCT	GAT I ATG GGCAAAAA TGT TTT AAA TTT CCA CCA CCT TTGC CCCT TCCA AAA	TCT L GAG TCTTTCA TCA TCA TGTT GAG GAT GGAT TCCG GGAT TCCCG CCG CCG CCG CCG CCG CCG CCG CCG	GGT V CTC TGA ATG TGG GCT TTA CCC AGG AAT TTG AAC CCT TTG TTGA TTG	GGA E ACG GCT TCT GCA ATT TAA CTC CCT TTTT CCC GCC CCAC CCA	GAC T TGT CAT AGT ATA TTC CCT GTC CAG CAC ATT AAC ATC CCA CTC TGC AGG CTC	900 237 960 1020 1080 1140 1260 1320 1380 1440 1500 1620 1680 1740 1800 1860 1920
901 961 1021 1081 1141 1201 1261 1321 1381 1441 1501 1661 1621 1681 1741 1801 1861	TTCCAC S T CTGAGA * GTTGTG TATCCT CTATTT TTTTGT TTAAAA AAATAC TCTACA TATGGT TAGGTC ACCAGT ACCAGT ACTGTC GCACCA AGAGAG TTTTAA GCTCCT GGCACCT	TTGC C GGCC CTTTC CTCA CTTA CTTCC CTAC CTA	ZAAG K ZACC CAGA CAG	TCTC S S CCA GAC. GAC. GAC. GAT. TTTT TTTT GTG GGC CTA GCA CCAT CGGG CCAT CGC CGG CCAT CGGG CCAT CGC CGG CCAT CGC CGG CCAT CGC CGG CCAT CGC CGC CGC CGC CGC CGC CGC CGC CGC CG	GACCO	CTGGG A GGCT FAAGG FTTT ACAA FTTT ACAA ATGC CTGT AGCA AGCA AGCT CGTT CGCC CCCTT	ETGA E AAGG CACT CCACT AAAC ACAT AAAC CCACT CCAC	GCTO L GGTG CTGTO CCTA CTTTT CCTT CCTT CGTT CGTA CTGT CGAA CTGG CTGA CTGG CTGG	GGAC D AGGC CCTI GGAC CTGC CTGC CATC	CCATA H CCAC AAGA AAGA AAGA CTGC CTGC CTGC CTGC CTTAAC CCTTAAC C	V V AGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GGTA V GTCO GGC TGTO AGA CCAT ACA CCGTO CCGG TCCC GAT TCT TCT TCT TCT TCT TCT TCT TCT TCT T	AGAGE ECCC. TCTG GTCG TTAGG GCT GCTG ACA GCT	GAT I ATG GGCACA TGT TTT AAA TTT CCA CCA CCT TGC CCCT TACA AAA GCT	TCT L GAG TCTTTCA TCA TCA TCA TCA TCA TCA TCA TCA	GGT V CTC TGA ATG GCT TTA AGG CCC GGC AAT TTG AAC CCT TTGA TTGA	GGA E ACG GCT TCT GCA ATT TAA CTC CCT TTT CCC GCC CAC CGTG CGTG	GAC T TGT CAT AGT ATA TTC CCT GTC CAC ATT AAC ATC CCA CTC TGC AGG CTC CTC CTC CTC CTC	900 237 960 1020 1080 1140 1260 1320 1380 1440 1500 1620 1680 1740 1860 1920 1980
901 961 1021 1081 1141 1201 1321 1381 1441 1501 1661 1621 1681 1741 1801 1861 1921 1981	TTCCAC S T CTGAGA * GTTGTG TATCCT CTATTT TTTTGT TTAAAA AAATAC TCTACA TATGGT TGGGTC ACCAGT ACTGTC GCACCA AGAGAG TTTTAA GCTCCT	TTGO C GGCO CTTTO CTTO CTTO CTTO CTTO CT	ZAAGA K ZACACACACACACACACACACACACACACACACACACAC	TCTCT S : CCA GAC. GAC. GAC. GAC. GAC. GAC. GAC. G	GACCO GACCO AGATTO AGGT AATTT TCTA TCTA AACT GTAC GATCO GTCA GCCA GTCA GCCA GTCA GCCA GTCA GCCA GC	CTGGC A GGCT FAAGC FTTT ACAA FTTT ACAA ATGC CTGT AGCA AGCA AGCA AGCA CGTT CGT CGTT CGT	ETGA E AAGG CACT ICAC CTTT AAAC ACAT AAAGG CACT GGTGT GTGG GTGT GTGA GTGA	GCTG L GTGTG CTAL CTTAG CTAL CTTTT CCTAL CTTTC CGTT CGAL CGCAG CTGAC CGGT CGGT CGGT CGGT CGGT CG	GGAC D AGGC CCT# GGAC CCT# CCTGC CCTTGC CCT	H CCAC H AAGA AAGA CTGC CTGC CTGC CTGC CTGC CTGC	rgt(V CCA(AGG(IGG' AGT' ITTA CTA(GAA) CCCA(GACC CCA CCA CCA CCA CCA CCA CCA CCA CC	GGTA V GTCO GGC GAT CAT CAT CAT CAT CAT CAT CAG	AGAGE E CCC. TCTG GTC, ATA TTTG GTG GCT GCT GCT GCT GCT GCT GCT GC	GAT I ATG GGCACA TGT TTT AAA TTT CCA CCA CCT TGC CCCT TACA AAA GCT	TCT L GAG TCTTTCA TCA TCA TCA TCA TCA TCA TCA TCA	GGT V CTC TGA ATG GCT TTA AGG CCC GGC AAT TTG AAC CCT TTGA TTGA	GGA E ACG GCT TCT GCA ATT TAA CTC CCT TTT CCC GCC CAC CGTG CGTG	GAC T TGT CAT AGT ATA TTC CCT GTC CAC ATT AAC ATC CCA CTC TGC AGG CTC CTC CTC CTC CTC	900 237 960 1020 1080 1140 1260 1320 1380 1440 1500 1620 1680 1740 1800 1860 1920

New U.S. Patent Application Inventors: R. JURECIC et al. Title: HEPP, A Novel Gene with a Role in Hematopoietic and Neural Development" Attorney Docket No. 39532.176599 Sheet 2of 14

FIGURE 1B

1 CGGGTCAGGACACAATGTTTGCACGAGGACTGAAGAGGAAATGTTGTTGGCCACGAGGAAG 1 M F A R G L K R K C V G H E E D 121 ACGTGGAGGAGCCCTGGCCGCTTGAAGACAGTGTCCTCATACAGCCTGCAGCGAGT 180 V E G A L A G L K T V S S Y S L Q R Q S 181 CGCTCCTGGACATGTCTCTGGTGAAGTTGCCACATGCTTGTGGAGCCCAACC L L D M S L V K L Q L C H M L V E P N L 181 TGTGCCGCTCAGTCCTCATTGCCAACACGGTCCGGCAGATCCAAGAGGAGATGACGCAGG C R S V L I A N T V R Q I Q E E M T Q D 182 T W R T V A P Q A A E R A P L D R L V 183 T E I L C R A A W G Q E G A H P A P G 184 AGGCACCAAGGCCCACACAGGGTCCAGGTCAGACAGTCCTCAGCACC 186 L G D G H T Q G P V S D L C P V T S A Q 187 GAAGCTTTCACAAGTCACCTGAGAGAGGAGATGACCAGG 186 A P R H L Q S S A W E M D G P R E N R G 186 GAAGCTTTCACAAGTCACTTGATCAGATATTTGAAACGCTGGAGACACAGGTACCAGCT 186 GAAGCTTTCACAAGTCACTTGATCAGATATTTGAAACGCTGGAGAAAAACCCCAGCT 186 GAAGCTTTCACAAGTCACTTGATCAGATATTTGAAACGCTGGAGACACAGGTACCTGAG 186 GAAGCTTTCACAAGTCACTTGATCAGATATTTGAAACGCTGGAGACACAGGTACCTGAG 186 GAAGCTTTCACAAGTCACTTGATCAGATATTTGAAACGCTGGAGACACAGGTACCTGAG 186 GAAGCTTTCACAAGTCACTTGATCAGATATTTGAAACGCTGGAGACACAGGTACTGA 186 GAAGCTTTCACAAGTCACTTGATCAGATATTTGAAACGCTGGACACAGGTACTGA 187 GAAGCTTTCACAAGTCACTTGATCAGATATTTGAAACGCTGGAGACACAGGTACTGA 187 G M M G G A R P G P C E G L E G L A P A 181 AGATCCTGTGGAGAGCAGCCCCTGGAGAGCCCTGGAGAGCCACAGGGTTGGCCCCTGGAGACCTGGAGCCCCTCGGAGCCCCTGGAGGCCTTGGACCACGTTGACCAGTTGACCCTTGACCAGGTTGACAGGTTGACAGGAGAGAGA
121 ACGTGGAGGAGCCCTGGCCGGCTTGAAGACAGTGTCCTCATACAGCCTGCAGCGGCAGT V E G A L A G L K T V S S Y S L Q R Q S 181 CGCTCCTGGACATGTCTCTGGTGAAGTTGCAGCTTTGCCACATGCTTGTGAGCCCCAACC L L D M S L V K L Q L C H M L V E P N L 241 TGTGCCGCTCAGTCCTCATTGCCAACACGGTCCGGCAGATCCAAGAGGGAGATGACGCAGG C R S V L I A N T V R Q I Q E E M T Q D 301 ATGGGACGTGGCGACAGTGGCACCCCAGGCTGCAGAGCGGGCGCGCTCGACCGCTTGG G T W R T V A P Q A A E R A P L D R L V 361 TCTCCACGGAGATCCTGTGCCGTGCAGCGTGGGGGCAAGAGGGGGCACATCCTGCTCCTG S T E I L C R A A W G Q E G A H P A P G 116 421 GCTTGGGGGACGCCACACACACAGGGTCCAGTTTCTGACCTTTGCCCAGTCACCTCAGCAC L G D G H T Q G P V S D L C P V T S A Q 136 481 AGGCACCAAGGCACCTGCAGAGCAGCGCCTGGAGAGAGGAGACACACCACACACA
V E G A L A G L K T V S S Y S L Q R Q S 368
181 CGCTCCTGGACATGTCTCTGGTGAAGTTGCAGCTTTGCCACATGCTTGTGAGCCCCAACC L L D M S L V K L Q L C H M L V E P N L 241 TGTGCCGCTCAGTCCTCATTGCCAACACGGTCCGGCAGATCCAAGAGGAGATGACGCAGG C R S V L I A N T V R Q I Q E E M T Q D 361 ATGGGACGTGCGCACAGTGCACCCCAGGCTGCAGAGAGGGGGGCCGCCGCTCGACCGCTTGG G T W R T V A P Q A A E R A P L D R L V 361 TCTCCACGGAGATCCTGTGCCGTGAGCGTGGGGGGCAAGAGGGGGGCACATCCTCGT S T E I L C R A A W G Q E G A H P A P G 421 GCTTGGGGGACGCCACACACAGGGTCCAGTTCTGACCTTTGCCCAGCACCTCTGCACCGCTTGACACACAC
L L D M S L V K L Q L C H M L V E P N L 241 TGTGCCGCTCAGTCCTCATTGCCAACACGGTCCGGCAGATCCAAGAGGAGATGACGCAGG C R S V L I A N T V R Q I Q E E M T Q D 301 ATGGGACGTGGCGCCACAGTGGCACCCCAGGCTGCAGAGCGGGCGCGCCGCTCGACCGCTTGG G T W R T V A P Q A A E R A P L D R L V 361 TCTCCACGGAGATCCTGTGCCGTGCAGCGGTGGGGGCAAGAGGGGGGCACATCCTGCTCCTG S T E I L C R A A W G Q E G A H P A P G 421 GCTTGGGGGACGCCACACACACAGGGTCCAGTTCTGACCTTTGCCCAGTCACCTCAGCAC L G D G H T Q G P V S D L C P V T S A Q 481 AGGCACCAAGGCACCTGCAGAGCAGCGCCTGGAGAGTGGACCCTCGAGAAAACAGAG A P R H L Q S S S A W E M D G P R E N R G 541 GAAGCTTTCACAAGTCACTTGATCAGATATTTGAAACGCTGGAGACTAAAAACCCCAGCT S F H K S L D Q I F E T L E T K N P S C 601 GCATGGAAGAGCTGTTCTCAGACGTGGACAGAGCCCCTTACACACAGTACTGA M E E L F S D V D S P Y Y D L D T V L T 196 661 CAGGCATGATGGGGGGTGCCAGGCCGGGGGCCCCTGGAAGAGGGGCTTGACCACAGTACTGA G M M G G A R P G P C E G L E G L A P A 721 CCACCCCAGGCCCTAGCTCCAGCTGCAAGTCCGACCTGGACCACAGTGGGC T P G P S S S C K S D L G E L D H V V V E 236
TGTGCCGCTCAGTCCTCATTGCCAACACGGTCCGGCAGATCCAAGAGGAGATGACGCAGG C R S V L I A N T V R Q I Q E E M T Q D 76 301 ATGGGACGTGGCGCACAGTGGCACCCCAGGCTGCAGAGGGGCGCCGCTCGACCGCTTGG 360 G T W R T V A P Q A A E R A P L D R L V 96 361 TCTCCACGGAGATCCTGTGCCGTGCAGCGTGGGGGGCAAGAGGGGGGCACATCCTGCTCCTG 420 S T E I L C R A A W G Q E G A H P A P G 110 421 GCTTGGGGGACGCCACACACACAGGGTCCAGTTTCTGACCTTTGCCCAGTCACCTCAGCAC 480 L G D G H T Q G P V S D L C P V T S A Q 130 481 AGGCACCAAGGCACCTGCAGAGCAGCGCCTGGAGATGGATG
C R S V L I A N T V R Q I Q E E M T Q D 76 301 ATGGGACGTGGCGCACAGTGGCACCCCAGGCTGCAGAGCGGGCGCGCTCGACCGCTTGG 366 G T W R T V A P Q A A E R A P L D R L V 96 361 TCTCCACGGAGATCCTGTGCCGTGCAGCGTGGGGGGCAAGAGGGGGCACATCCTGCTCCTG 426 S T E I L C R A A W G Q E G A H P A P G 116 421 GCTTGGGGGACGCCACACACAGGGTCCAGTTTCTGACCTTTGCCCAGTCACCTCAGCAC 486 L G D G H T Q G P V S D L C P V T S A Q 136 481 AGGCACCAAGGCACCTGCAGAGCAGCGCCTGGGAGATGGATG
301 ATGGGACGTGGCGCACAGTGGCACCCCAGGCTGCAGAGCGGGCGCCGCTCGACCGCTTGG G T W R T V A P Q A A E R A P L D R L V 361 TCTCCACGGAGATCCTGTGCCGTGCAGCGTGGGGGGCAAGAGGGGGGCACATCCTGCTCCTG S T E I L C R A A W G Q E G A H P A P G 116 421 GCTTGGGGGACGCCACACACAGGGTCCAGTTCTGTACCTTTGCCCAGTCACCTCAGCAC L G D G H T Q G P V S D L C P V T S A Q 136 481 AGGCACCAAGGCACCTGCAGAGCAGCGCCTTGGAGATGGACCCTCAGCAC A P R H L Q S S A W E M D G P R E N R G 541 GAAGCTTTCACAAGTCACTTGATCAGATATTTGAAACGCTGGAGACTAAAAACCCCAGCT S F H K S L D Q I F E T L E T K N P S C 601 GCATGGAAGAGCTGTTCTCAGACGTGGACAGGCCCTTACTACGACCTGGACACAGTACTGA M E E L F S D V D S P Y Y D L D T V L T 196 661 CAGGCATGATGGGGGGTGCCAGGCCCGGGCCCTGCGAAGGGCTTGGCTCCGG G M M G G A R P G P C E G L E G L A P A 216 721 CCACCCCAGGCCCTAGCTCCAGCTGCAAGTCCGACCTGGGCGAGCCACGTGGTGG T P G P S S S C K S D L G E L D H V V E 236
G T W R T V A P Q A A E R A P L D R L V 361 TCTCCACGGAGATCCTGTGCCGTGCAGCGTGGGGGCAAGAGGGGGGCACATCCTGCTCCTG S T E I L C R A A W G Q E G A H P A P G 421 GCTTGGGGGACGCCACACACAGGGTCCAGTTCTGACCTTTGCCCAGTCACCTCAGCAC L G D G H T Q G P V S D L C P V T S A Q 481 AGGCACCAAGGCACCTGCAGAGCAGCGCCTGGGAGATGGATG
361 TCTCCACGGAGATCCTGTGCCGTGCAGCGTGGGGGCAAGAGGGGGCACATCCTGCTCCTG S T E I L C R A A W G Q E G A H P A P G 421 GCTTGGGGGACGCCACACACAGGGTCCAGTTTCTGACCTTTGCCCAGTCACCTCAGCAC L G D G H T Q G P V S D L C P V T S A Q 481 AGGCACCAAGGCACCTGCAGAGCAGCGCCTGGGAGATGGATG
S T E I L C R A A W G Q E G A H P A P G 421 GCTTGGGGGACGCCACACACAGGGTCCAGTTCTGACCTTTGCCCAGTCACCTCAGCAC L G D G H T Q G P V S D L C P V T S A Q 481 AGGCACCAAGGCACCTGCAGAGCAGCGCCTGGGAGATGGATG
421 GCTTGGGGGACGCCACACACAGGGTCCAGTTTCTGACCTTTGCCCAGTCACCTCAGCAC L G D G H T Q G P V S D L C P V T S A Q 481 AGGCACCAAGGCACCTGCAGAGCAGCGCCTGGGAGATGGATG
L G D G H T Q G P V S D L C P V T S A Q 136 481 AGGCACCAAGGCACCTGCAGAGCAGCGCCTGGGAGATGGATG
481 AGGCACCAAGGCACCTGCAGAGCAGCGCCTGGGAGATGGATG
A P R H L Q S S A W E M D G P R E N R G 156 541 GAAGCTTTCACAAGTCACTTGATCAGATATTTGAAACGCTGGAGACTAAAAACCCCAGCT 606 S F H K S L D Q I F E T L E T K N P S C 176 601 GCATGGAAGAGCTGTTCTCAGACGTGGACAGCCCCTACTACGACCTGGACACAGTACTGA 666 M E E L F S D V D S P Y Y D L D T V L T 196 661 CAGGCATGATGGGGGGTGCCAGGCCGGGCCCCTGCGAAGGGCTCGAGGGCTTGGCTCCGG 726 G M M G G A R P G P C E G L E G L A P A 216 721 CCACCCCAGGCCCTAGCTCCAGCTGCAAGTCCGACCTGGACCACGTGGTGG 786 T P G P S S S C K S D L G E L D H V V E 236
541 GAAGCTTTCACAAGTCACTTGATCAGATATTTGAAACGCTGGAGACTAAAAACCCCAGCT S F H K S L D Q I F E T L E T K N P S C 601 GCATGGAAGAGCTGTTCTCAGACGTGGACAGCCCCTACTACGACCTGGACACAGTACTGA M E E L F S D V D S P Y Y D L D T V L T 661 CAGGCATGATGGGGGGTGCCAGGCCCGGGCCCCTGCGAAGGGCTCGAGGGCTTGGCTCCGG G M M G G A R P G P C E G L E G L A P A 721 CCACCCCAGGCCCTAGCTCCAGCTGCAAGTCCGACCTGGACCACGTGGTGG T P G P S S S C K S D L G E L D H V V E 236
S F H K S L D Q I F E T L E T K N P S C 176 601 GCATGGAAGAGCTGTTCTCAGACGTGGACAGCCCCTACTACGACCTGGACACAGTACTGA 666 M E E L F S D V D S P Y Y D L D T V L T 196 661 CAGGCATGATGGGGGGTGCCAGGCCGGGCCCCTGCGAAGGGCTCGAGGGCTTGGCTCCGG 726 G M M G G A R P G P C E G L E G L A P A 216 721 CCACCCCAGGCCCTAGCTCCAGCTGCAAGTCCGACCTGGGCGAGCTGGACCACGTGGTGG 786 T P G P S S S C K S D L G E L D H V V E 236
601 GCATGGAAGAGCTGTTCTCAGACGTGGACAGCCCCTACTACGACCTGGACACAGTACTGA M E E L F S D V D S P Y Y D L D T V L T 661 CAGGCATGATGGGGGGTGCCAGGCCGGGCCCCTGCGAAGGGCTCGAGGGCTTGGCTCCGG G M M G G A R P G P C E G L E G L A P A 721 CCACCCCAGGCCCTAGCTCCAGCTGCAAGTCCGACCTGGGCGAGCTGGACCACGTGGTGG T P G P S S S C K S D L G E L D H V V E 236
M E E L F S D V D S P Y Y D L D T V L T 196 661 CAGGCATGATGGGGGGTGCCAGGCCGGGCCCCTGCGAAGGGCTCGAGGGCTTGGCTCCGG G M M G G A R P G P C E G L E G L A P A 216 721 CCACCCCAGGCCCTAGCTCCAGCTGCAAGTCCGACCTGGGCGAGCTGGACCACGTGGTGG T P G P S S S C K S D L G E L D H V V E 236
661 CAGGCATGATGGGGGGTGCCAGGCCGGGCCCTGCGAAGGGCTCGAGGGCTTGGCTCCGG G M M G G A R P G P C E G L E G L A P A 210 721 CCACCCCAGGCCCTAGCTCCAGCTGCAAGTCCGACCTGGGCGAGCTGGACCACGTGGTGG T P G P S S S C K S D L G E L D H V V E 230
G M M G G A R P G P C E G L E G L A P A 210 721 CCACCCCAGGCCCTAGCTCCAGCTGCAAGTCCGACCTGGGCGAGCTGGACCACGTGGTGG T P G P S S S C K S D L G E L D H V V E 230
721 CCACCCCAGGCCCTAGCTCCAGCTGCAAGTCCGACCTGGGCGAGCTGGACCACGTGGTGG T P G P S S S C K S D L G E L D H V V E 23
TPGPSSCKSDLGELDHVVE 23
I L V E T * 24 841 ACACGTGAGCACTGGCTCCCACGGAGGGTGCGCCTGCCGCCAGCCCTGCCGCCAGCCTTGCTGC 90
9.01 CCTGTCTGCTGATTCTGAGAAATCCCAGAACAGCCCATTACCAGTGGGGCTGCAGCCTA 96
961 GGCCGTCCCACTCACCTCCCCCTGTGGAGCGCCAGAGAGGCTGTTCTGGAAGGCTT 102
100
1021 CTTGTCTTCTGACGTCCCCACAGCCCTGGGCCCCTCGTGTCTCTTTGTGTCCCCCACTGT 108 1081 AGAGGACGGTGAGCCGCAGCTGCATCAACCTCCTTTTACCTTTAGATAGGTGAATTTTTA 114
1081 AGAGGACGGTGAGCCGCAGCTGCATCAACCTCCTTTTACCTTTAGATAGGTGAATTTTTT 120 1141 CAATTCAGTTTTACATGTTTTTGGGCAGTATTTTTGTCTTAAGATATATTTTTTTAAACTTTT 120
1201 TATACCTTATCTCTTTAGATTTTTTCAGCTATTTTCTTAAAAGTATATTTTTTTT
1201 TATACCTTATCTCTTTAGATTTTTTCAGCTATTTTCTTAAAACTATTTTTTTCTATAAACTATTTTTCTATAAACTATTTTTCTATAAACTATTTTTCTATAAACTATTTTTCTATAAACTATTTTCTATAAACTATTTTTT
1321 TTTTTTTAAGGTTTAAATAAGGGTTTTTTGTTTTGTTT
1381 TACAGTCTCAGTCAACAGTGTGAATGTATCATGTTTTACTTTAAATGTGTGTG
1441 TCTTCATTATGTCCTGCGCTGCAGTGAGACCTGGGTGAAAATCAGGAGCCGCACACAGCC 150
1501 ACATCTTCCTAGACCTAAGAGTAAATTATGGAGGATTTTATTTA
1561 AATGTCATTGAAGACAAAGGTCAAATATTTGTCTGTTTGTAGATCACAGGCACCAGTTGG 162
1621 TCTTCAGGGACCTCATAGCCCCTCGGTGGTGCCTTCTCAAGGCAGTGTTCCTGGAGGCTC 168
1681 CCATCAGGGTCAGCCCATGCACCTGCCCTGGGTGAGGAAGTAGCATTGCTGCTGGATGAG 174
1741 AAACGCCTGCGCTGCTCTGTTAGACTGGTGCTGAAACAAAAGGTTAAGGCTAGGTTGAAG 180
1801 TCTAGAATGAAAGAAATCTGAATCCATGTCATTCATAACCCCTTGATCTGTAGTGTCATG 186
1861 GGTGCTGCCGCAGGCAGGGAGTGAGCTGGGGGTGCCTGCAGCCTTCCACTCCTGCCCCGC 192
1921 CTCACCCCACATGCTCCCTGTTTCTCATGCTTTCTCTAACTTCCTCACCCCTTAACCAAA 198
1981 AAGGTGTGTTTTCTTTTGTGCATATAGCCATTCTTAAATATCAGTGATGTAAACCTCACT 204
2041 TTATTAAAAATTATCCAGCAAAAAAAAAAAAAAAAAAAA

Title: HEPP, A Novel Gene with a R Hematopoietic and Neural Developme Attorney Docket No. 39532.176599

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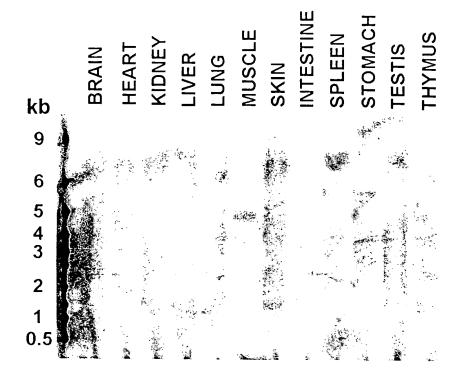
FIGURE 2

Mouse Human	 1	MFARGLKRK <mark>YGD</mark> OEEGY <mark>EGFGTVP</mark> SYSLQRQSLLDMSLVKLQLCHMLVEPNLCRSV MFARGLKRK <mark>CVGHEEDVEGALAG</mark> LK <mark>TVS</mark> SYSLQRQSLLDMSLVKLQLCHMLVEPNLCRSV
Mouse	 57	LIANTVRQIQEEMSQDGVWHGMAPQNVDRAPVERLVSTEILCRTVRGAEEEHPAPELEDA
Human	61	LIANTVRQIQEEMTQDGTWRTVAPQAAERAPLDRLVSTEILCRAAWGQEGAHPAPGLGDG
Mouse	 117	PLONSVSELPIVGSAPGORNPOSSIWEMDSPOENRGSFOKSLDOIFETLENKNSSSVEEL
Human	121	HTOGPVSDLCPVTSAOAPRHLOSSAWEMDGPRENRGSFHKSLDOIFETLETKNPSGMEEL
Mouse	 177	FSDVDSSYYDLDTVLTGMMSGTKSSLCNGLEGFAAATPPPSSTCKSDLAELDHVVEILVE
Human	181	FSDVDSPYYDLDTVLTGMMGGARPGPCEGLEGLAPATPGPSSSCKSDLGELDHVVEILVE
Mouse Human	 237 241	

Zebrafish Hepp Mouse Hepp Human HEPP	1	MF <mark>SKG</mark> IKRKFADGGEEISDDGLVAARVASSYSLQRQSLLDMSLIKLQLCHMLVEPNLCRS MFARGLKRKYGDOEEGVEGFGTVPSYSLQRQSLLDMSLVKLQLCHMLVEPNLCRS MFARGLKRKCVGH-EEDVEGALAGLKTVSSYSLQRQSLLDMSLVKLQLCHMLVEPNLCRS
Zebrafish Hepp	61	VLIANTVRQIQEEMTHDGSWHMVTEAFCGASQSPSERLVETEVLCR
Mouse Hepp	56	VLIANTVRQIQEEMSQDGVWHGMAPQNVDRAPWERLVSTEILCRTVRGAEEEHPAPEL
Human HEPP	60	VLIANTVRQIQEEMTQDGTWRTVAPQAAER APIADRLVSTEILCRAAWGQEGAHPAPGL

FIGURE 4B

New U.S. Patent Application Inventors: R. JURECIC et al. Title: HEPP, A Novel Gene with a Role Hematopoietic and Neural Development" Attorney Docket No. 39532.176599 Sheet 4 of 14



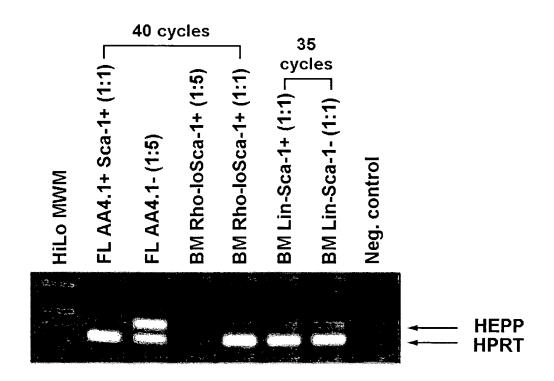
BRAIN
HEART
KIDNEY
LIVER
LUNG
MUSCLE
SKIN
INTESTINE
SPLEEN
SPLEEN
STOMACH
TESTIS



FIGURE 4A

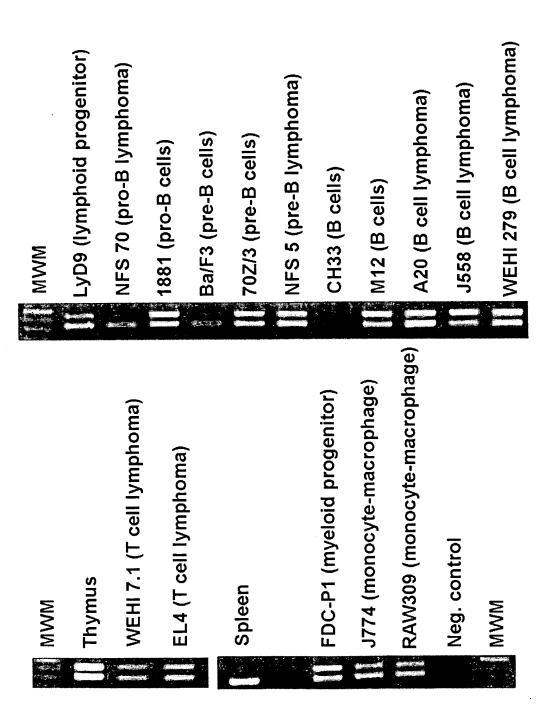
FIGURE 5

New U.S. Patent Application
Invent R. JURECIC et al.
Title P, A Novel Gene with a Role in
Hematopoietic and Neural Development"
Attorney Docket No. 39532.176599
Sheet 5 of 14



New U.S. Patent Application Inventors: R. JURECIC et al. Title: HEPP, A Novel Gene with a Role in Hematopoietic and Neural Development" Attorney Docket No. 39532.176599

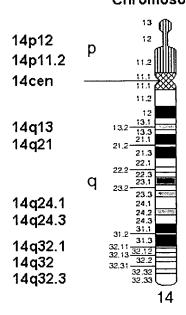
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New U.S. Patent Application Inventors: R. JURECIC et al. Title: HEPP, A Novel Gene with a Roll-Hematopoietic and Neural Development" Attorney Docket No. 39532.176599 Sheet 7 of 14

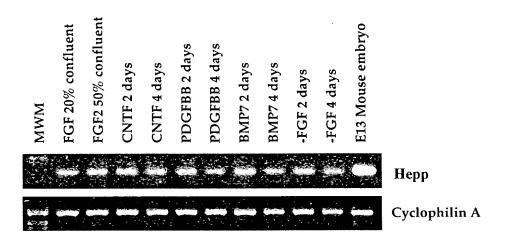
FIGURE 7

Chromosome 14



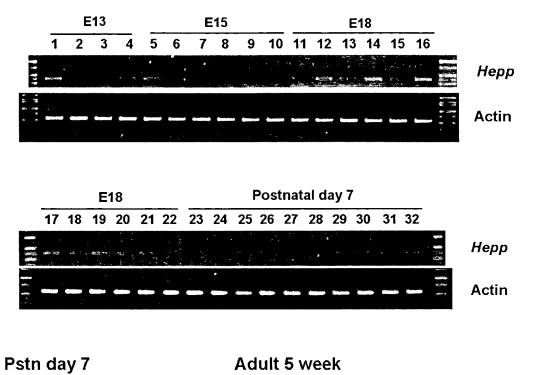
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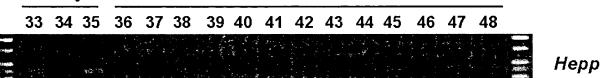
New U.S. Patent Application
Inventors: R. JURECIC et al.
Title: HEPP, A Novel Gene with a Romatopoietic and Neural Development"
Attorney Docket No. 39532.176599
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New U.S. Patent Application
Inventors: R. JURECIC et al.
Title: HEPP, A Novel Gene with a RoHematopoietic and Neural Development"
Attorney Docket No. 39532.176599

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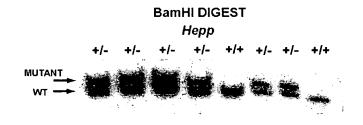


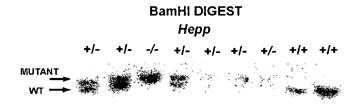


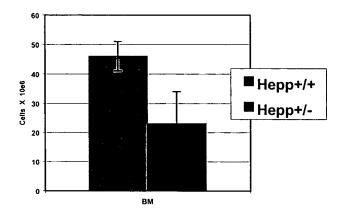
Embryo day 13	Embryo day 18	Postnatal day 7	Adult 5 week
1. Telencephalon/Diencephalon	11. Frontal cortex	23. Frontal cortex	36. Frontal cortex
2. Mesescephalon (Micorzin)	12. Posterior cortex	24. Posterior cortex	37. Posterior contex
3. Rhombescephalon (Hindbrain)	13. Entochinal conex	25. Entochinal cortex	38. Entorinal cores:
4. Spinal cord	14. Offsctory balb	26. Olfactory bulb	39; Offactory bulb
a. Span sees	15. Hippocampus	27. Hippocampos	40. Ніррэсатрия
Embryo day 15	16. Striatum	28. Striaturn	41. Striatum
5. Telenocephalon	17. Thalames	29. Thalames	42. Thalarous
•	18. Hypothalamus	30. Hypothalamus	43. Hypothalamus
6. Dienoephalon	19. Midbrain	31. Cerebellum	44, Cerebellum
7. Midbrain	20. Pocs	32. Michrain	45, Midbrain
8. Pons	21. Medula	33. Pocs	46. Pecs
9. Medulia	22. Spinal cord	34. Medralia	47. Medulla
10. Spinzi cord	zz. spanie wio	35 Soinal cord	48 Seinzt cord

New U.S. Patent Application
Inventors: R. JURECIC et al.
Title: HEPP, A Novel Gene with a Role in
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FIGURE 10







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FIGURE 12

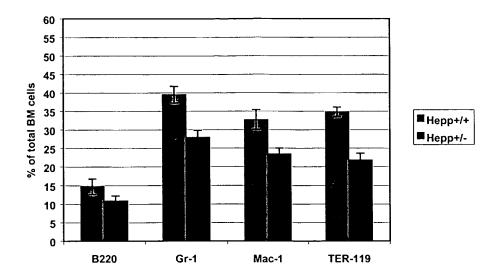
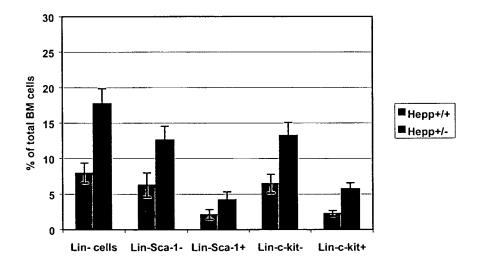


FIGURE 13



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FIGURE 14

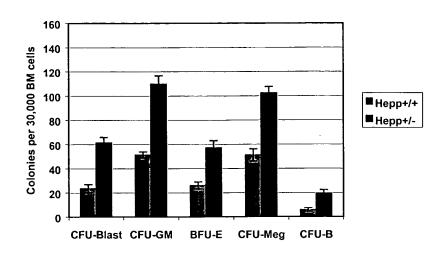
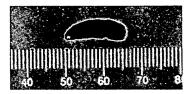


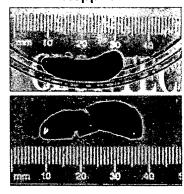
FIGURE 15A-B

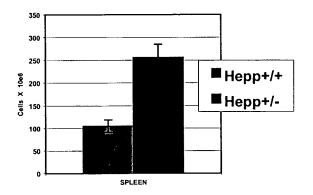
FIGURE 15C

Hepp +/+

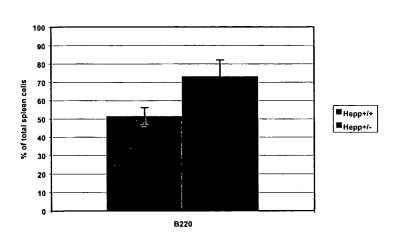


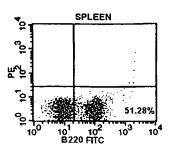
Hepp +/-





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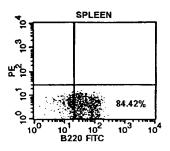
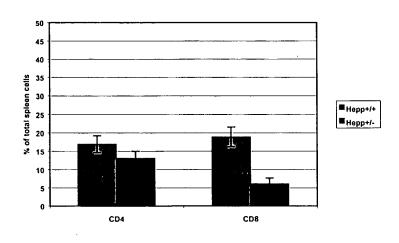
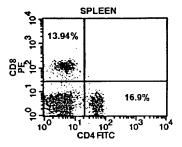
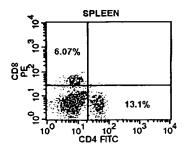


FIGURE 17









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FIGURE 18A



FIGURE 18B



FIGURE 18C

